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No. PN 7276 for a patent by THE WALTER AND ELIZA HALL INSTITUTE OF
MEDICAL RESEARCH filed on 22 December 1995.

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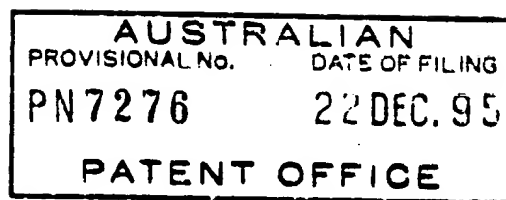
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PROVISIONAL SPECIFICATION
for the invention entitled:

"A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING
SAME - II"

The invention is described in the following statement:

**A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME - II**

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The present invention relates generally to a novel haemopoietin receptor or components or parts thereof and to genetic sequences encoding same. The receptor molecules and their components and/or parts and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists,
10 therapeutics and diagnostic reagents based on ligand interaction with its receptor.

Bibliographic details of the publications numerically referred to in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide and amino acid sequences referred to in the specification are defined
15 following the bibliography.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers but not the
20 exclusion of any other integer or group of integers.

The rapidly increasing sophistication of recombinant DNA techniques is greatly facilitating research into the medical and allied health fields. Cytokine research is of particular importance, especially as these molecules regulate the proliferation,
25 differentiation and function of a wide variety of cells. Administration of recombinant cytokines or regulating cytokine function and/or synthesis is becoming increasingly the focus of medical research into the treatment of a range of disease conditions.

Despite the discovery of a range of cytokines and other secreted regulators of cell
30 function, comparatively few cytokines are directly used or targeted in therapeutic regimens. One reason for this is the pleiotropic nature of many cytokines. For example, interleukin (IL)-11 is a functionally pleiotropic molecule (1,2), initially

characterized by its ability to stimulate proliferation of the IL-6-dependent plasmacytoma cell line, T11 65 (3). Other biological actions of IL-11 include induction of multipotential haemopoietin progenitor cell proliferation (4,5,6), enhancement of megakaryocyte and platelet formation (7,8,9,10), stimulation of acute phase protein synthesis (11) and inhibition of adipocyte lipoprotein lipase activity (12, 13).

Interleukin-13 (IL-13) is another important cytokine which shares a number of structural characteristics with interleukin-4 (IL-4) [reviewed in 14 and 15]. The genes for IL-4 and IL-13 have a related intron/exon structure and are located close together on chromosome 5 in the human and the syntenic region of chromosome 11 in the mouse (14, 15). At the protein level, IL-4 and IL-13 share approximately 30% amino acid identity, including four cysteine residues. Biologically, IL-13 and IL-4 are also similar, being produced by activated T-cells and acting upon macrophages to induce differentiation and suppress the production of inflammatory cytokines. Additionally, human IL-13 may act as a co-stimulatory signal for B-cell proliferation and affect immunoglobulin isotype switching (14, 15). The diverse and pleiotropic function of IL-13 and other haemopoietic cytokine makes this molecule an important group to study, especially at the level of interaction of the cytokine with its receptors. Manipulation and control of cytokine receptors and of cytokine-receptor interaction is potentially very important in many therapeutic situations, especially where the target cytokine is functionally pleiotropic and it is desired to block certain functions of a target cytokine but not all functions.

Research into IL-13 and its receptor has been hampered due to the inability to clone genetic sequences encoding all or part of the IL-13 receptor. In accordance with the present invention, genetic sequences have now been cloned encoding the IL-13 receptor α -chain. The availability of these genetic sequences permits the development of a range of therapeutic and diagnostic agents capable of modulating IL-13 activity as well as the activity of cytokines related at the level of IL-13 receptor structure.

Accordingly, one aspect of the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding an haemopoietin receptor α -chain from an animal or a component, fragment, part, derivative, homologue or analogue thereof.

More particularly, the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding the IL-13 receptor α -chain from an animal or a component, fragment, part, derivative, homologue or analogue thereof.

In a related embodiment, the present invention contemplates a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding the IL-4 receptor α -chain from an animal or a component, fragment, part, derivative, homologue or analogue thereof.

Preferably, the animal is a mammal or a species of bird. Particularly, preferred mammals include humans, laboratory test animals (e.g. mice, rabbits, guinea pigs), livestock animals (e.g. sheep, horse, pigs, cows), companion animals (e.g. dogs, cats) or captive wild animals (e.g. kangaroos). Although the present invention is exemplified with respect to mice and humans, the scope of the subject invention extends to all animals and birds.

The present invention is predicated in part on an ability to identify members of the haemopoietin receptor family on the basis of sequence similarity. Based on this approach, a genetic sequence was identified in accordance with the present invention which encodes the IL-13 α -chain. The expressed genetic sequence is referred to herein as "NR4". NR4 has an apparent molecular weight when synthesised by transfected COS cells of from about 50,000 to about 70,000 daltons, and more preferably from about 55,000 to about 65,000 daltons. NR4 binds to IL-13 with low affinity and is considered, therefore, to be IL-13 receptor α -chain. Accordingly, the terms "NR4" and IL-13 receptor α -chain" (or "IL-13 R α ") are used interchangeably throughout the subject

specification. Furthermore, in accordance with the present invention, IL-13 binding to its receptor has been found to be competitively inhibited by IL-4 or a component thereof which may provide a method for controlling IL-13-receptor interaction and which may also provide a basis for the preparation and construction of mimetics.

5

Another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding IL-13 receptor α -chain having an amino acid sequence as set forth in SEQ ID NO:2 or having at least about 50% similarity to all or part thereof. Preferably, the percentage similarity is at least about 60%, more preferably at
10 least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

A further embodiment of the present invention contemplates a nucleic acid molecule comprising a sequence of nucleotides encoding the IL-13 receptor α -chain and having
15 a nucleotide sequence substantially as set forth in SEQ ID NO:1 or having at least about 50% similarity to all or part thereof. Preferably, the percentage similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

20 Still another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding IL-13 receptor α -chain having an amino acid sequence as set forth in SEQ ID NO:4 or having at least about 50% similarity to all or part thereof. Preferably, the percentage similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more
25 preferably at least about 90-95% or greater.

Yet still a further embodiment of the present invention contemplates a nucleic acid molecule comprising a sequence of nucleotides encoding the IL-13 receptor α -chain and having a nucleotide sequence substantially as set forth in SEQ ID NO:3 or having at
30 least about 50% similarity to all or part thereof. Preferably, the percentage similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

Accordingly, the present invention extends to the sequence of nucleotides set forth in SEQ ID NO:1 or 3 or the sequence of amino acids set forth in SEQ ID NO:2 or 4 or single or multiple nucleotide or amino acid substitutions, deletions and/or additions thereto.

5

The present invention further extends to nucleic acid molecules capable of hybridising under low stringency conditions to the nucleotide sequence set forth in SEQ ID NO:1 or 3 or a complementary form thereof.

- 10 For the purposes of defining the level of stringency, reference can conveniently be made to Maniatis *et al* (1982) at pages 387-389 which are incorporated herein by reference where the washing step at paragraph 11 is considered herein to be high stringency. A low stringency wash is defined herein to be 0.1-0.2xSSC, 0.1% w/v SDS at 55-65°C for 20 minutes and a medium level of stringency is considered herein to be 2xSSC, 15 0.1% w/v SSC at $\geq 45^{\circ}\text{C}$ for 20 minutes. The alternative conditions are applicable depending on concentration, purity and source of nucleic acid molecules.

- Yet another aspect of the present invention provides a nucleic acid molecule comprising a sequence of nucleotides which encodes or is complementary to a sequence which 20 encodes an IL-13 receptor α -chain, said nucleic acid molecule having a nucleotide sequence substantially as set forth in SEQ ID NO:1 or 3 or a nucleic acid molecule which encodes a structurally similar IL-13 receptor α -chain or a derivative thereof and which is capable of hybridising to the nucleotide sequence substantially as set forth in SEQ ID NO:1 or 3 or a complementary form thereof under low stringency conditions.

25

- Still yet another aspect of the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides which encodes or is complementary to a sequence which encodes the IL-13 receptor α -chain having an amino acid sequence substantially as set forth in SEQ ID NO:2 or 4 or comprises a nucleotide sequence coding for an 30 amino acid sequence having at least about 50% similarity to the sequence set forth in SEQ ID NO:2 or 4 and is capable of hybridising to the sequence set forth in SEQ ID NO:1 or 3 under low stringency conditions.

The nucleic acid molecules contemplated by the present invention are generally in isolated form and are preferably cDNA or genomic DNA molecules. In a particularly preferred embodiment, the nucleic acid molecules are in vectors and most preferably expression vectors to enable expression in a suitable host cell. Particularly useful host
5 cells include prokaryotic cells, mammalian cells, yeast cells and insect cells. The cells may also be in the form of a cell line.

According to this aspect of the present invention there is provided an expression vector comprising a nucleic acid molecule encoding the IL-13 receptor α -chain as hereinbefore
10 described, said expression vector capable of expression in a particularly host cell.

Another aspect of the present invention contemplates a recombinant polypeptide comprising a sequence of amino acids substantially as set forth in SEQ ID NO:2 or 4 or having at least about 50% similarity to all or part thereof. Preferably, the percentage
15 similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

The recombinant polypeptide contemplated by the present invention includes, therefore,
20 components, parts, fragments, derivatives, homologues or analogues of the IL-13 receptor α -chain and is preferably encoded by a nucleotide sequence substantially set forth in SEQ ID NO:1 or 3 or a molecule having at least about 50% similarity to all or part thereof or a molecule capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:1 or 3 or a complementary form thereof. The recombinant molecule may
25 be glycosylated or non-glycosylated. When in glycosylated form, the glycosylation may be substantially the same as naturally occurring IL-13 receptor α -chain or may be a modified form of glycosylation. Altered or differential glycosylation states may or may not affect binding activity of the IL-13 receptor α -chain.

30 The recombinant IL-13 receptor α -chain may be in soluble form or may be expressed on a cell surface or conjugated or fused to a solid support or another molecule.

The present invention extends to chemical analogues of the recombinant IL-13 receptor α -chain.

- Chemical analogues of the recombinant IL-13 receptor α -chain contemplated herein
- 5 include, but are not limited to, modifications to side chains, incorporation of unnatural amino acids and/or their derivatives during peptide synthesis and the use of crosslinkers and other methods which impose conformational constraints on the peptides or their analogues.
- 10 Examples of side chain modifications contemplated by the present invention include modifications of amino groups such as by reductive alkylation by reaction with an aldehyde followed by reduction with NaBH_4 ; amidination with methylacetimidate; acylation with acetic anhydride; carbamoylation of amino groups with cyanate;
- 15 trinitrobenzylation of amino groups with 2, 4, 6, trinitrobenzene sulphonic acid (TNBS); acylation of amino groups with succinic anhydride and tetrahydrophthalic anhydride; and pyridoxylation of lysine with pyridoxal-5'-phosphate followed by reduction with NaBH_4 .

- The guanidine group of arginine residues may be modified by the formation of
- 20 heterocyclic condensation products with reagents such as 2,3-butanedione, phenylglyoxal and glyoxal.

- The carboxyl group may be modified by carbodiimide activation *via* O-acylisourea formation followed by subsequent derivitisation, for example, to a corresponding amide.
- 25

- Sulphydryl groups may be modified by methods such as carboxymethylation with iodoacetic acid or iodoacetamide; performic acid oxidation to cysteic acid; formation of a mixed disulphides with other thiol compounds; reaction with maleimide, maleic anhydride or other substituted maleimide; formation of mercurial derivatives using 4-
- 30 chloromercuribenzoate, 4-chloromercuriphenylsulphonic acid, phenylmercury chloride, 2-chloromercuri-4-nitrophenol and other mercurials; carbamoylation with cyanate at alkaline pH.

Tryptophan residues may be modified by, for example, oxidation with N-bromosuccinimide or alkylation of the indole ring with 2-hydroxy-5-nitrobenzyl bromide or sulphenyl halides. Tyrosine residues on the other hand, may be altered by nitration with tetranitromethane to form a 3-nitrotyrosine derivative.

5

Modification of the imidazole ring of a histidine residue may be accomplished by alkylation with iodoacetic acid derivatives or N-carbethoxylation with diethylpyrocarbonate.

- 10 Examples of incorporating unnatural amino acids and derivatives during peptide synthesis include, but are not limited to, use of norleucine, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 6-aminohexanoic acid, t-butylglycine, norvaline, phenylglycine, ornithine, sarcosine, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine and/or D-isomers of amino acids.

15

Crosslinkers can be used, for example, to stabilise 3D conformations, using homo-bifunctional crosslinkers such as the bifunctional imido esters having $(CH_2)_n$ spacer groups with $n=1$ to $n=6$, glutaraldehyde, N-hydroxysuccinimide esters and hetero-bifunctional reagents which usually contain an amino-reactive moiety such as N-
20 hydroxysuccinimide and another group specific-reactive moiety such as maleimido or dithio moiety (SH) or carbodiimide (COOH). In addition, peptides can be conformationally constrained by, for example, incorporation of C_α and N_α -methylamino acids, introduction of double bonds between C_α and C_β atoms of amino acids and the formation of cyclic peptides or analogues by introducing covalent bonds such as forming
25 an amide bond between the N and C termini, between two side chains or between a side chain and the N or C terminus.

- Chemical modification of the recombinant IL-13 receptor α -chain may be important, for example, to increase serum half-life, to protect the molecule from enzymatic degradation
30 and/or for diagnostic purposes.

The recombinant IL-13 receptor α -chain contemplated by the present invention is useful in the development of a range of agonists and antagonists of IL-13-receptor interaction. The recombinant molecule may also be used in the development of diagnostic agents.

5

Particularly useful agents encompassed by this aspect of the present invention are antibodies to the recombinant IL-13 receptor α -chain. The antibodies may be monoclonal or polyclonal and are particularly useful as antagonists of IL-13-receptor binding or as diagnostic agents to qualitate or quantitate the presence of the IL-13
10 receptor α -chain. These antibodies may also be useful in the screening of similar components in other receptors such as IL-4 receptors.

Other agonists and antagonists include chemical molecules which, for example, structurally, functionally or electrochemically mimic or have similarities to IL-13
15 receptor α -chain or which comprise a solubilised form of the IL-13 receptor α -chain.

Such agents are useful in modulating IL-13-receptor interaction and these are useful in enhancing or diminishing IL-13 related activities. This may be particularly important for cancers or tumours involving or resulting from excess IL-13 or from aberrant IL-13
20 molecules or to promote IL-13 function in the treatment of a range of conditions such as, but not limited to, immune deficiency.

The present invention further contemplates ribozyme and antisense molecules useful in reducing IL-13 receptor α -chain expression.

25

The present invention encompasses, therefore, pharmaceutical and diagnostic compositions comprising recombinant IL-13 receptor α -chain or parts thereof, antibodies thereto, agonists or antagonists thereof or genetic molecules such as ribozymes, antisense molecules and constructs useful in co-suppression.

30

The present invention is further described by the following non-limiting Figures and Examples.

5 In the Figures:

Figure 1 is a representation of the nucleotide [SEQ ID NO:1] and predicted amino acid [SEQ ID NO:2] sequence of murine NR4. The untranslated region is shown in lower case and the translated region in upper case. The conventional one-letter code for amino acids is employed, potential asparagine linked glycosylation sites are underlined and the conserved cysteine residues and WSXWS motif of haemopoietin receptor family members are shown in bold. The predicted signal sequence is underlined in bold while the transmembrane domain is underlined with dashes. The sequence shown is a composite derived from the analysis of 8 cDNA clones derived from 3 libraries. The 5'-end of the sequence (nucleotides -60 to 351) is derived from a single cDNA clone but is also present in genomic DNA clones that have been isolated.

Figure 2 is a photographic representation showing northern analysis of murine NR4 mRNA expression in selected tissues and organs.

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Figure 3 is a graphical representation depicting saturation isotherms of ^{125}I -IL-13 and ^{125}I -IL-4 binding; saturation isotherms depicted as Scatchard plots of IL-4 (○) and IL-13 (●) binding to (A) COS cells expressing the IL-13R α (NR4), (B) CTLL cells and (C) CTLL cells expressing the IL-13R α (NR4). Data have been normalised to 1×10^4 COS cells and 1×10^6 CTLL cells and binding was carried out on ice for 2 to 4 hours.

25

Figure 4 is a graphical representation showing specificity of IL-4 and IL-13 binding; the ability of IL-4 (○) and IL-13 (●) to compete for ^{125}I -IL-13 binding to (A) COS cells expressing the IL-13R α (NR4) and (C) CTLL cells expressing the IL-13R α (NR4) or to compete for IL-4 binding to (B) CTLL cells and (D). CTLL cells expressing the IL-13R α (NR4) binding was carried out on ice for 2 to 4 hours and the data have been expressed as a percentage of the specific binding observed in the absence of a competitor

30

(■).

Figure 5 is a graphical representation showing factor dependent proliferation of cells expressing NR4. Two hundred (A) CTLL cells or (B) CTLL cells expressing the IL-13R α (NR4) were incubated in the absence of cytokine (■) or with various concentrations of IL-2 (□), IL-4 (○) or IL-13 (●). After 48 hours viable cells were counted and data was expressed as a percentage of the number of viable cells observed with a maximal concentration of IL-2.

Figure 6 is a photographic representation showing cross-species conservation of NR4 (IL-13R α) gene.

Figure 7 is a representation of the nucleotide and corresponding amino acid sequence of murine and human NR4 (IL-13R α) genes. The nucleotide and predicted amino acid sequence of human (H) and murine (M) IL-13R α (NR4) were aligned by eye, with gaps (-) inserted to optimise the alignment. The numbering is for the murine clone, nucleotides that form part of the coding region are shown in upper case, whilst those of the untranslated regions are shown in lower case. Amino acids identical between the predicted murine and human proteins are indicated by (*). DNA encoding the murine signal sequence is underlined, with A26 or T27 being the predicted first amino acid of the mature protein.

Figure 8 is a photographic representation showing NR4 expression in mouse tissues.

The following single and three letter abbreviations for amino acid residues are used in the specification:

5			
	Amino Acid	Three-letter Abbreviation	One-letter Symbol
	Alanine	Ala	A
10	Arginine	Arg	R
	Asparagine	Asn	N
	Aspartic acid	Asp	D
	Cysteine	Cys	C
	Glutamine	Gln	Q
15	Glutamic acid	Glu	E
	Glycine	Gly	G
	Histidine	His	H
	Isoleucine	Ile	I
	Leucine	Leu	L
20	Lysine	Lys	K
	Methionine	Met	M
	Phenylalanine	Phe	F
	Proline	Pro	P
	Serine	Ser	S
25	Threonine	Thr	T
	Tryptophan	Trp	W
	Tyrosine	Tyr	Y
	Valine	Val	V
	Any residue	Xaa	X
30			

EXAMPLE 1

Isolation of genomic and cDNAs encoding NR4

ApoI digested genomic DNA, extracted from an embryonal stem cell line, was cloned
5 into the λ ZAPII bacteriophage (Stratagene, LaJolla, CA). Approximately 10^6 plaques
from this library were screened with a ^{32}P -labelled oligonucleotide corresponding to the
sequence Trp-Ser-Asp-Trp-Ser [SEQ ID NO:3] (16). Positively hybridising clones were
sequenced using an automated DNA sequencer according to the manufacturer's
instructions (Applied Biosystems, Foster City, CA). One clone appeared to encode for
10 part of a new member of the haemopoietin receptor family. Oligonucleotides were
designed on the basis of this genomic DNA sequence and were used in the conventional
manner to isolate clones from mouse peritoneal macrophage (Clontech Laboratories, Palo
Alto, CA), mouse skin, mouse lung, mouse kidney, and WEHI-3B (Stratagene, LaJolla,
CA) λ -bacteriophage cDNA libraries.

15

EXAMPLE 2

Construction of expression vectors and transfection of cells

Using PCR, a derivative of the NR4 cDNA was generated which encoded for the IL-3
signal sequence and an N-terminal FLAG epitope-tag preceding the mature coding
20 region of NR4 (Thr27 to Pro424; Figure 1). The PCR product was cloned into the
mammalian expression vector pEF-BOS (17). Constructs were sequenced in their
entirety prior to use. Cells were transfected and selected as previously described (16,
18).

25

EXAMPLE 3

Northern blots

Northern blots were performed as previously described (16). The source of hybridisation
probes was as follows: NR4 - a PCR product from nucleotide 32 to 984 (Figure 1) and
GAPDH - a cDNA fragment spanning nucleotides (19) [REF REQUIRED].

30

EXAMPLE 4

Cytokines and binding experiments using radioiodinated cytokines

IL-2, IL-4, IL-7, IL-9, IL-13 and IL-15 were obtained commercially (R & D Systems, Minneapolis MN). For radioiodination, cytokines were dissolved at a concentration of 100 µg/ml in 10 mM sodium phosphate, 150 mM NaCl (PBS), 0.02% v/v Tween 20 and 0.02% w/v sodium azide at pH 7.4. An amount of 2µg of IL-13 was radioiodinated using the iodine monochloride method (20, 21), while 2µg of IL-4 was radiolabelled using diiodo-Bolton-Hunter reagent (16). Binding studies and determination of the specific radioactivity and bindability of labelled cytokines were performed as previously described (2).

EXAMPLE 5

Proliferation Assays

The proliferation of Ba/F3 and CTLL cells in response to cytokines was measured in Lux 60 microwell HL-A plates (Nunc Inc. IL, USA). Cells were washed three times in DME containing 20% v/v new born calf serum and resuspended at a concentration of 2×10^4 cells per ml in the same medium. Aliquots of 10µl of the cell suspension were placed in the culture wells with 5µl of various concentrations of purified recombinant cytokines. After 2 days of incubation at 37°C in a fully humidified incubator containing 10% v/v CO₂ in air, viable cells were counted using an inverted microscope.

EXAMPLE 6

Cloning and Characterisation of Murine NR4

A library was constructed in λZAPII using *ApoI* digested genomic DNA from embryonal stem cells and screened with a pool of ³²P-labelled oligonucleotides encoding the amino acid sequence Trp-Ser-Asp-Trp-Ser [SEQ ID NO:3] found in many members of the haemopoietin receptor family. One hybridising bacteriophage was found to contain a genomic clone that appeared to encode part of a novel member of the haemopoietin receptor family. This receptor was given the operational name NR4. The sequence of the genomic clone was used to isolate cDNAs encoding NR4 from WEHI-3B cell, peritoneal macrophage, bone marrow, skin and kidney libraries. A composite of the

nucleotide sequence [SEQ ID NO:1] and predicted amino acid sequence [SEQ ID NO:2] of these cDNAs is shown in Figure 1. The NR4 cDNA is predicted to encode for a protein of 424 amino acid residues, containing a putative signal sequence and transmembrane domain. The extracellular region of the protein containing a putative
5 signal sequence and transmembrane domain. The extracellular region of the protein contained an immunoglobulin-like domain (amino acids 27-117), in addition to a typical haemopoietin receptor domain (amino acids 118-340) which includes four conserved cysteine residues and the characteristic Trp-Ser-Asp-Trp-Ser [SEQ ID NO:3] motif (Figure 1). The cytoplasmic tail of the new receptor was 60 amino acids in length.

10

EXAMPLE 7

Expression pattern of NR4 cDNA

The pattern of NR4 mRNA expression was examined by Northern analyses. Two hybridising species of 5.2 and 2.2 kb in length were detected in mRNA from most
15 tissues (Figure 2). NR4 mRNA was not detectable in skeletal muscle (Figure 2). Figure 8 shows expression of NR4 in mouse tissues.

EXAMPLE 8

NR4 encodes the IL-13 receptor α -chain (IL-13R α) - a specific

20 **binding subunit of the IL-13 receptor**

The apparent molecular weight is from about 50,000 to about 70,000 daltons and more particularly about 55,000 to about 65,000 daltons for NR4 expressed in COS cells estimated from Western blots using an anti-FLAG antibody, suggested that NR4 might encode the binding subunit of the IL-13 receptor. In order to test this possibility NR4
25 was expressed in COS cells. Untransfected COS cells expressed relatively low levels of IL-4 and IL-13 receptors. Upon transfection with a plasmid containing the NR4 cDNA, the number of IL-13 receptors but not IL-4 receptors expressed by COS cells was dramatically increased (Figure 3A; 100,000 to 500,000 receptors per cell). The affinity of IL-13 for NR4 expressed by COS cells was low ($K_D \sim 2-10$ nM) and binding
30 was specific since it was in competition with unlabelled IL-13 but not other cytokines including IL-2, IL-4, IL-7, IL-9 or IL-15 (Figure 4A). These results suggest that NR4 is the IL-13 receptor α -chain (IL-13R α).

EXAMPLE 9

The IL-13R α (NR4) and the IL-4R α are shared components of the IL-4 and IL-3 receptors

In order to investigate the relationship between IL-4 and IL-13 receptors, the IL-4 responsive cell line CTLL was examined. Parental CTLL cells expressed a single class of IL-4 receptor ($K_D \sim 660$ pM; ~ 3600 receptors per cell) but no detectable IL-13 receptors (Figure 3B). The IL-4 receptors expressed by CTLL cells appeared to be specific since binding of ^{125}I -IL-4 was in competition with unlabelled IL-4 but not IL-13 (Figure 4B). Upon expression of the IL-13R α (NR4) in CTLL cells no change was observed in the number or affinity of IL-4 receptors, while a single class of high affinity IL-13 receptors was detected (Figure 3C; $K_D \sim 75$ pM; 1350 receptors per cell). The affinity of IL-13 for the IL-13R α (NR4) expressed in CTLL cells was higher than in COS cells, suggesting that the former expressed a protein capable of interacting with the IL-13R α (NR4) to increase the affinity for IL-13. A likely candidate based on previous studies is the IL-4R α . In order to explore this possibility the ability of IL-4 to compete with ^{125}I -IL-13 for binding to CTLL cells expressing the IL-13R α (NR4) was assessed. Figure 4B shows that IL-4 and IL-13 were equally effective in competing for ^{125}I -IL-13 binding ($\text{IC}_{50} \sim 300$ pM; Figure 4C) and, in addition, were able to compete with ^{125}I -IL-4 for binding ($\text{IC}_{50} \sim 300$ pM; Figure 4D).

20

EXAMPLE 10

Expression of the IL-13R α (NR4) is necessary for transduction of a proliferative signal by IL-13

CTLL cells require the addition of exogenous cytokines for survival and proliferation. IL-2 was found to be a potent proliferative stimulus for CTLL cells ($\text{EC}_{50} \sim 100$ -200 pM), while IL-4 was relatively weak (EC_{50} 2-7 nM) and IL-13 was inactive (Figure 5A). Expression of the IL-13R α (NR4) in CTLL cells resulted in the ability to survive and proliferate weakly in response to IL-13 ($\text{EC}_{50} \sim 700$ pM) and to proliferate somewhat more strongly than parental cells in response to IL-4 ($\text{EC}_{50} \sim 700$ pM; Figure 5B).

30

EXAMPLE 11

Cloning of Human IL-13R α (NR4)

In order to determine whether genes homologous to murine IL-13R α (NR4) exist in
5 other vertebrate species, a probe encompassing nucleotides 840 to 1270 of murine IL-
13R α (NR4) was hybridised to *Eco*RI digested genomic DNA from various species.
Hybridisation was carried out in 500 mM Na₂HPO₄ (~5xSSC) at 50°C overnight. The
filter was washed in 40 mM Na₂HPO₄ (~0.2xSSC) at 50°C for 2 hours and exposed to
autoradiographic film for 48 hours. Figure 6 illustrates that relatively few (1 to 5)
10 hybridising bands are observed in genomic DNA from various species, including human.
This suggests that it is feasible to clone human IL-13R α (NR4) using a murine cDNA
probe. A human bone marrow cDNA library clones in the λ ZAPII bacteriophage was
therefore screened with two probes (nucleotides 82-840 and 840 to 1270) from the
murine IL-13R α (NR4) cDNA. Hybridisation was carried out overnight in 6xSSC, 0.1%
15 w/v SDS at 42°C. Filters were washed at 2xSSC, 0.1% w/v SDS at 50°C for 2 hours
and exposed for 48 hours to autoradiographic film. Plaques that hybridised to both
murine IL-13R α (NR4) probes were picked and purified in the conventional manner.
The cDNA inserts from the hybridising bacteriophage were excised into the pBluescript
plasmid and sequenced in their entirety using an ABI automated sequencer. Figure 7
20 shows a composite of the sequence of the clones isolated and reveals that the clones
encode a protein that shares a high degree of sequence similarity with murine IL-13R α
(NR4). The clones encode for the entire mature coding region of the protein, but lack
the initiation methionine and the signal sequence; the high degree of sequence similarity
(311/401 amino acids ~ 78%) predicates that this cDNA is the human homologue of the
25 murine IL-13R α (NR4).

Those skilled in the art will appreciate that the invention described herein is susceptible
to variations and modifications other than those specifically described. It is to be
understood that the invention includes all such variations and modifications. The
30 invention also includes all of the steps, features, compositions and compounds referred
to or indicated in this specification, individually or collectively, and any and all
combinations of any two or more of said steps or features.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE WALTER AND ELIZA HALL INSTITUTE OF
MEDICAL RESEARCH
- (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND
GENETIC SEQUENCES ENCODING SAME - II
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIES COLLISON CAVE
 - (B) STREET: 1 LITTLE COLLINS STREET
 - (C) CITY: MELBOURNE
 - (D) STATE: VICTORIA
 - (E) COUNTRY: AUSTRALIA
 - (F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: AU PROVISIONAL
 - (B) FILING DATE: 23-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HUGHES DR, E JOHN L
 - (C) REFERENCE/DOCKET NUMBER: EJH/EK
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: +61 3 9254 2777
 - (B) TELEFAX: +61 3 9254 2770

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TGAAAAGATA GAATAAATGG CCTCGTGCCG AATTCGGCAC GAGCCGAGGC GAGGGCCTGC      -1
ATG GCG CGG CCA GCG CTG CTG GGC GAG CTG TTG GTG CTG CTA CTG TGG      48
Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
  1           5           10           15
ACC GCC ACC GTG GGC CAA GTT GCC GCG GCC ACA GAA GTT CAG CCA CCT      96
Thr Ala Thr Val Gly Gln Val Ala Ala Thr Glu Val Gln Pro Pro
          20           25           30
GTG ACG AAT TTG AGC GTC TCT GTC GAA AAT CTC TGC ACG ATA ATA TGG      144
Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
          35           40           45
ACG TGG AGT CCT CCT GAA GGA GCC AGT CCA AAT TGC ACT CTC AGA TAT      192
Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
          50           55           60
TTT AGT CAC TTT GAT GAC CAA CAG GAT AAG AAA ATT GCT CCA GAA ACT      240
Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
          65           70           75           80
CAT CGT AAA GAG GAA TTA CCC CTG GAT GAG AAA ATC TGT CTG CAG GTG      288
His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
          85           90           95
GGC TCT CAG TGT AGT GCC AAT GAA AGT GAG AAG CCT AGC CCT TTG GTG      336
Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
          100          105          110
AAA AAG TGC ATC TCA CCC CCT GAA GGT GAT CCT GAG TCC GCT GTG ACT      384
Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr
          115          120          125
GAG CTC AAG TGC ATT TGG CAT AAC CTG AGC TAT ATG AAG TGT TCC TGG      432
Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
          130          135          140
CTC CCT GGA AGG AAT ACA AGC CCT GAC ACA CAC TAT ACT CTG TAC TAT      480
Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
          145          150          155          160
TGG TAC AGC AGC CTG GAG AAA AGT CGT CAA TGT GAA AAC ATC TAT AGA      528
Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
          165          170          175
GAA GGT CAA CAC ATT GCT TGT TCC TTT AAA TTG ACT AAA GTG GAA CCT      576
Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
          180          185          190
AGT TTT GAA CAT CAG AAC GTT CAA ATA ATG GTC AAG GAT AAT GCT GGG      624
Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
          195          200          205

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AAA ATT AGG CCA TCC TGC AAA ATA GTG TCT TTA ACT TCC TAT GTG AAA Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys 210 215 220	672
CCT GAT CCT CCA CAT ATT AAA CAT CTT CTC CTC AAA AAT GGT GCC TTA Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu 225 230 235 240	720
TTA GTG CAG TGG AAG AAT CCA CAA AAT TTT AGA AGC AGA TGC TTA ACT Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr 245 250 255	768
TAT GAA GTG GAG GTC AAT AAT ACT CAA ACC GAC CGA CAT AAT ATT TTA Tyr Glu Val Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu 260 265 270	816
GAG GTT GAA GAG GAC AAA TGC CAG AAT TCC GAA TCT GAT AGA AAC ATG Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met 275 280 285	864
GAG GGT ACA AGT TGT TTC CAA CTC CCT GGT GTT CTT GCC GAC GCT GTC Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val 290 295 300	912
TAC ACA GTC AGA GTA AGA GTC AAA ACA AAC AAG TTA TGC TTT GAT GAC Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp 305 310 315 320	960
AAC AAA CTG TGG AGT GAT TGG AGT GAA GCA CAG AGT ATA GGT AAG GAG Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu 325 330 335	1008
CAA AAC TCC ACC TTC TAC ACC ACC ATG TTA CTC ACC ATT CCA GTC TTT Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe 340 345 350	1056
GTC GCA GTG GCA GTC ATA ATC CTC CTT TTT TAC CTG AAA AGG CTT AAG Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys 355 360 365	1104
ATC ATT ATA TTT CCT CCA ATT CCT GAT CCT GGC AAG ATT TTT AAA GAA Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu 370 375 380	1152
ATG TTT GGA GAC CAG AAT GAT GAT ACC CTG CAC TGG AAG AAG TAT GAC Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp 385 390 395 400	1200
ATC TAT GAG AAA CAA TCC AAA GAA GAA ACG GAT TCT GTA GTG CTG ATA Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile 405 410 415	1248
GAA AAC CTG AAG AAA GCA GCT CCT TGATGGGGAG AAGTGATTTC TTTCTTGCCT Glu Asn Leu Lys Lys Ala Ala Pro 420	1302
TCAATGTGAC CCTGTGAAGA TTTATTGCAT TCTCCATTTG TTATCTGGGG GACTTGTTAA	1362
ATAGAAACTG AAACACTCT TGAAAAACAG GCAGCTCCTA AGAGCCACAG GTCTTGATGT	1422
GACTTTTGCA TTGAAAACCC AAACCCAAAG GAGCTCCTTC CAAGAAAAGC AAGAGTTCTT	1482
CTCGTTCCTT GTTCCAATCC CTAAAAGCAG ATGTTTTGCC AAATCCCCAA ACTAGAGGAC	1542
AAAGACAAGG GGACAATGAC CATCAATTCA TCTAATCAGG AATTGTGATG GCTTCCTAAG	1602
GAATCTCTGC TTGCTCTG	1620

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 amino acids
 (P) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1           5           10           15
Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro
          20           25           30
Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
          35           40           45
Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
          50           55           60
Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
          65           70           75           80
His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
          85           90           95
Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
          100          105          110
Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr
          115          120          125
Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
          130          135          140
Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
          145          150          155          160
Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
          165          170          175
Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
          180          185          190
Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
          195          200          205
Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys
          210          215          220
Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu
          225          230          235          240
Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr
          245          250          255
Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu
          260          265          270
Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
          275          280          285
Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
          290          295          300
Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp
          305          310          315          320

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Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Cln Ser Ile Gly Lys Glu
325 330 335
Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
340 345 350
Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
355 360 365
Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
370 375 380
Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
385 390 395 400
Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile
405 410 415
Glu Asn Leu Lys Lys Ala Ala Pro
420

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCG	CCT	ACG	GAA	ACT	CAG	CCA	CCT	GTG	ACA	AAT	TTG	AGT	GTC	TCT	GTT	48
Ala	Pro	Thr	Glu	Thr	Gln	Pro	Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	
1				5				10						15		
GAA	AAC	CTC	TGC	ACA	GTA	ATA	TGG	ACA	TGG	AAT	CCA	CCC	GAG	GGA	GCC	96
Glu	Asn	Leu	Cys	Thr	Val	Ile	Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	
			20					25					30			
AGC	TCA	AAT	TGT	AGT	CTA	TGG	TAT	TTT	AGT	CAT	TTT	GGC	GAC	AAA	CAA	144
Ser	Ser	Asn	Cys	Ser	Leu	Trp	Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	
		35					40					45				
GAT	AAG	AAA	ATA	GCT	CCG	GAA	ACT	CGT	CGT	TCA	ATA	GAA	GTA	CCC	CTG	192
Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	
	50					55					60					
AAT	GAG	AGG	ATT	TGT	CTG	CAA	GTG	GGG	TCC	CAG	TGT	AGC	ACC	AAT	GAG	240
Asn	Glu	Arg	Ile	Cys	Leu	Gln	Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	
	65				70					75					80	
AGT	GAG	AAG	CCT	AGC	ATT	TTG	GTT	GAA	AAA	TGC	ATC	TCA	CCC	CCA	GAA	288
Ser	Glu	Lys	Pro	Ser	Ile	Leu	Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	
				85					90					95		
GGT	GAT	CCT	GAG	TCT	GCT	GTG	ACT	GAA	CTT	CAA	TGC	ATT	TGG	CAC	AAC	336
Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	
		100						105					110			
CTG	AGC	TAC	ATG	AAG	TGT	TCT	TGG	CTC	CCT	GGA	AGG	AAT	ACC	AGT	CCC	384
Leu	Ser	Tyr	Met	Lys	Cys	Ser	Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	
		115					120				125					
GAC	ACT	AAC	TAT	ACT	CTC	TAC	TAT	TGG	CAC	AGA	AGC	CTG	GAA	AAA	ATT	432
Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile		
	130					135					140					
CAT	CAA	TGT	GAA	AAC	ATC	TTT	AGA	GAA	GGC	CAA	TAC	TTT	GGT	TGT	TCC	480
His	Gln	Cys	Glu	Asn	Ile	Phe	Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	
	145				150					155					160	
TTT	GAT	CTG	ACC	AAA	GTG	AAG	GAT	TCC	AGT	TTT	GAA	CAA	CAC	AGT	GTC	528
Phe	Asp	Leu	Thr	Lys	Val	Lys	Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	
				165					170					175		
CAA	ATA	ATG	GTC	AAG	GAT	AAT	GCA	GGA	AAA	ATT	AAA	CCA	TCC	TTC	AAT	576
Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	
			180					185					190			
ATA	GTG	CCT	TTA	ACT	TCC	CGT	GTG	AAA	CCT	GAT	CCT	CCA	CAT	ATT	AAA	624
Ile	Val	Pro	Leu	Thr	Ser	Arg	Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	
		195					200					205				
AAC	CTC	TCC	TTC	CAC	AAT	GAT	GAC	CTA	TAT	GTG	CAA	TGG	GAG	AAT	CCA	672
Asn	Leu	Ser	Phe	His	Asn	Asp	Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	
	210					215					220					

CAG Gln 225	AAT Asn 225	TTT Phe 225	ATT Ile 225	AGC Ser 225	AGA Arg 230	TGC Cys 230	CTA Leu 230	TTT Phe 230	TAT Tyr 235	GAA Glu 235	GTA Val 235	GAA Glu 235	GTC Val 235	AAT Asn 240	AAC Asn 240	720
AGC Ser 245	CAA Gln 245	ACT Thr 245	GAG Glu 245	ACA Thr 245	CAT His 245	AAT Asn 245	GTT Val 245	TTC Phe 250	TAC Tyr 250	GTC Val 250	CAA Gln 255	GAG Glu 255	GCT Ala 255	AAA Lys 255	TGT Cys 255	768
GAG Glu 260	AAT Asn 260	CCA Pro 260	GAA Glu 260	TTT Phe 260	GAG Glu 265	AGA Arg 265	AAT Asn 265	GTG Val 265	GAG Glu 265	AAT Asn 270	ACA Thr 270	TCT Ser 270	TGT Cys 270	TTC Phe 270	ATG Met 270	816
GTC Val 275	CCT Pro 275	GGT Gly 275	GTT Val 275	CTT Leu 275	CCT Pro 280	GAT Asp 280	ACT Thr 280	TTG Leu 280	AAC Asn 280	ACA Thr 285	GTC Val 285	AGA Arg 285	ATA Ile 285	AGA Arg 285	GTC Val 285	864
AAA Lys 290	ACA Thr 290	AAT Asn 290	AAG Lys 290	TTA Leu 290	TGC Cys 295	TAT Tyr 295	GAG Glu 295	GAT Asp 295	GAC Asp 295	AAA Lys 300	CTC Leu 300	TGG Trp 300	AGT Ser 300	AAT Asn 300	TGG Trp 300	912
AGC Ser 305	CAA Gln 305	GAA Glu 305	ATG Met 305	AGT Ser 310	ATA Ile 310	GGT Gly 310	AAG Lys 310	AAG Lys 310	CGC Arg 315	AAT Asn 315	TCC Ser 315	ACA Thr 315	CTC Leu 315	TAC Tyr 320	ATA Ile 320	960
ACC Thr 325	ATG Met 325	TTA Leu 325	CTC Leu 325	ATT Ile 325	GTT Val 325	CCA Pro 325	GTC Val 330	ATC Ile 330	GTC Val 330	GCA Ala 330	GGT Gly 330	GCA Ala 335	ATC Ile 335	ATA Ile 335	GTA Val 335	1008
CTC Leu 340	CTG Leu 340	CTT Leu 340	TAC Tyr 340	CTA Leu 340	AAA Lys 340	AGG Arg 340	CTC Leu 345	AAG Lys 345	ATT Ile 345	ATT Ile 345	ATA Ile 345	TTC Phe 350	CCT Pro 350	CCA Pro 350	ATT Ile 350	1056
CCT Pro 355	GAT Asp 355	CCT Pro 355	GGC Gly 355	AAG Lys 355	ATT Ile 355	TTT Phe 360	AAA Lys 360	GAA Glu 360	ATG Met 360	TTT Phe 365	GGA Gly 365	GAC Asp 365	CAG Gln 365	AAT Asn 365	GAT Asp 365	1104
GAT Asp 370	ACT Thr 370	CTG Leu 370	CAC His 370	TGG Trp 370	AAG Lys 375	AAG Lys 375	TAC Tyr 375	GAC Asp 375	ATC Ile 375	TAT Tyr 380	GAG Glu 380	AAG Lys 380	CAA Gln 380	ACC Thr 380	AAG Lys 380	1152
GAG Glu 385	GAA Glu 385	ACC Thr 385	GAC Asp 385	TCT Ser 390	GTA Val 390	GTG Val 390	CTG Leu 390	ATA Ile 390	GAA Glu 395	AAC Asn 395	CTG Leu 395	AAG Lys 395	AAA Lys 395	GCC Ala 400	TCT Ser 400	1200
CAG Gln 1248	TGA Gln 1248	TGG Gln 1248	AGA Gln 1248	TAA Gln 1248	TTT Gln 1248	ATT Gln 1248	TTT Gln 1248	ACC Gln 1248	TTC Gln 1248	ACT Gln 1248	GTG Gln 1248	ACC Gln 1248	TTG Gln 1248	AGA Gln 1248	AGA Gln 1248	1248

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val
1 5 10 15
Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala
20 25 30
Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln
35 40 45
Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu
50 55 60
Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Thr Asn Glu
65 70 75 80
Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu
85 90 95
Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn
100 105 110
Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro
115 120 125
Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile
130 135 140
His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser
145 150 155 160
Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val
165 170 175
Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn
180 185 190
Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys
195 200 205
Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro
210 215 220
Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn
225 230 235 240
Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys
245 250 255
Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met
260 265 270
Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val
275 280 285
Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp
290 295 300
Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile
305 310 315 320

Thr	Met	Leu	Leu	Ile	Val	Pro	Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val
				325					330					335	
Leu	Leu	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile
			340					345					350		
Pro	Asp	Pro	Gly	Lys	Ile	Phe	Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp
		355					360					365			
Asp	Thr	Leu	His	Trp	Lys	Lys	Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys
	370					375					380				
Glu	Glu	Thr	Asp	Ser	Val	Val	Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser
385					390					395					400
Gln															

DATED this 22nd day of December, 1995

THE WALTER AND ELIZA HALL INSTITUTE
OF MEDICAL RESEARCH

By Its Patent Attorneys

DAVIES COLLISON CAVE

1 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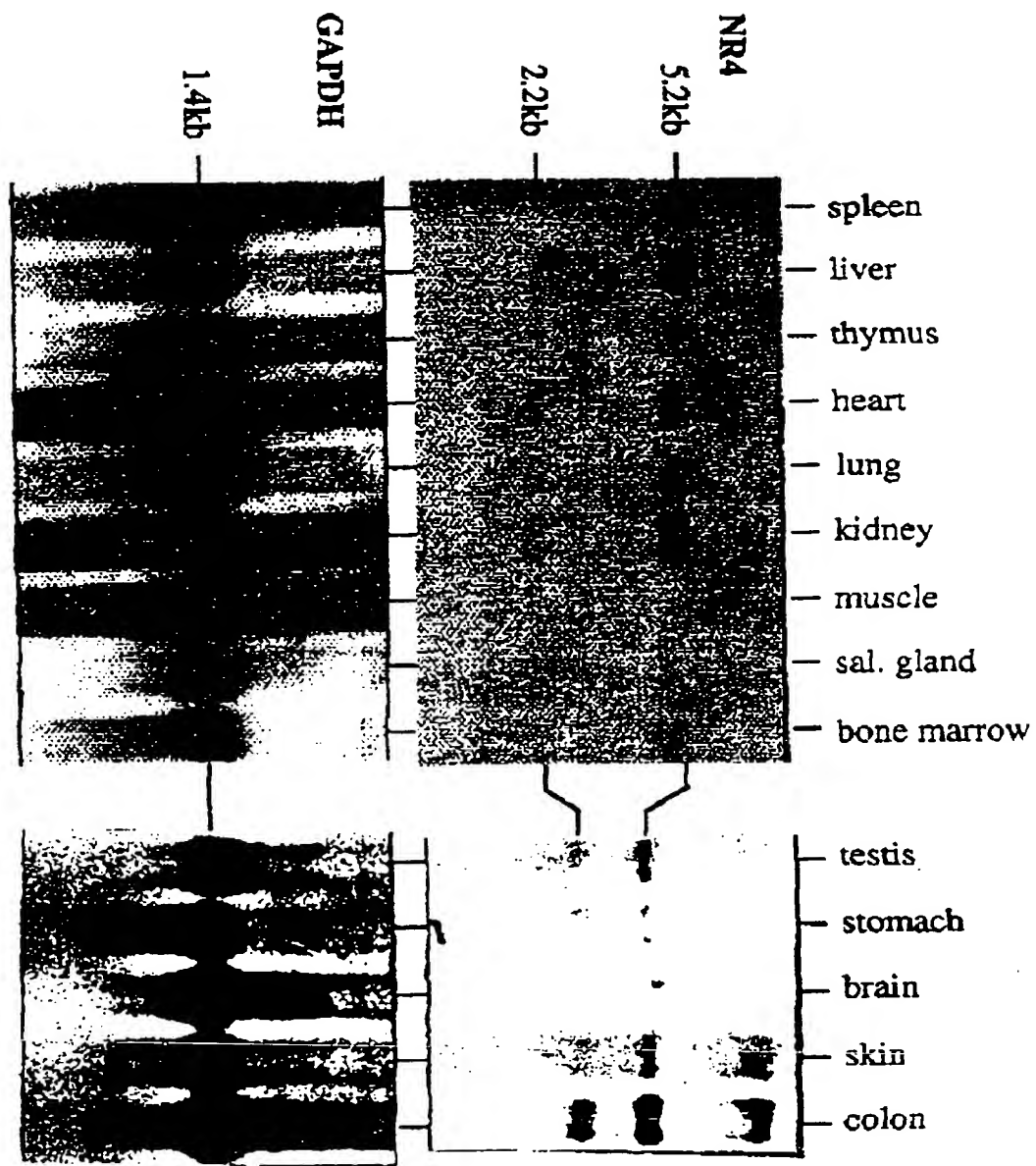


FIGURE 2

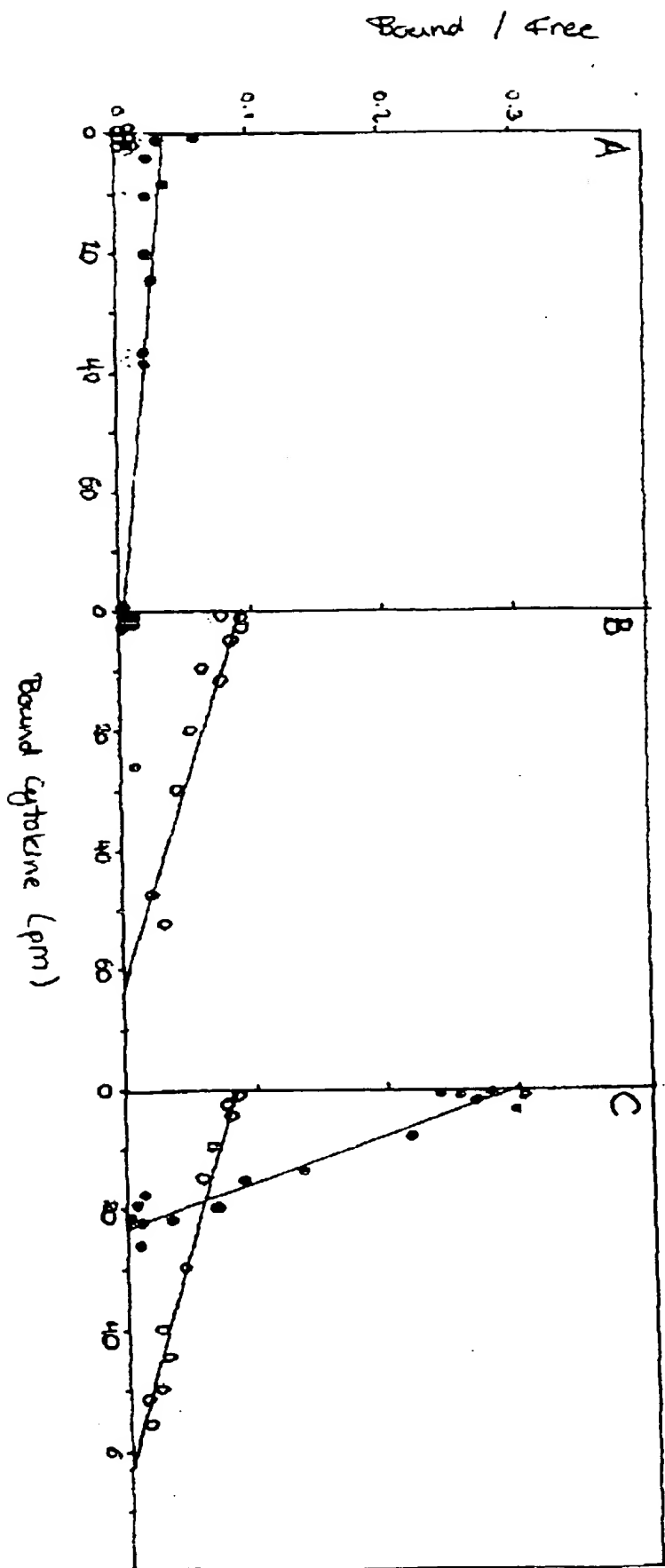


FIGURE 3

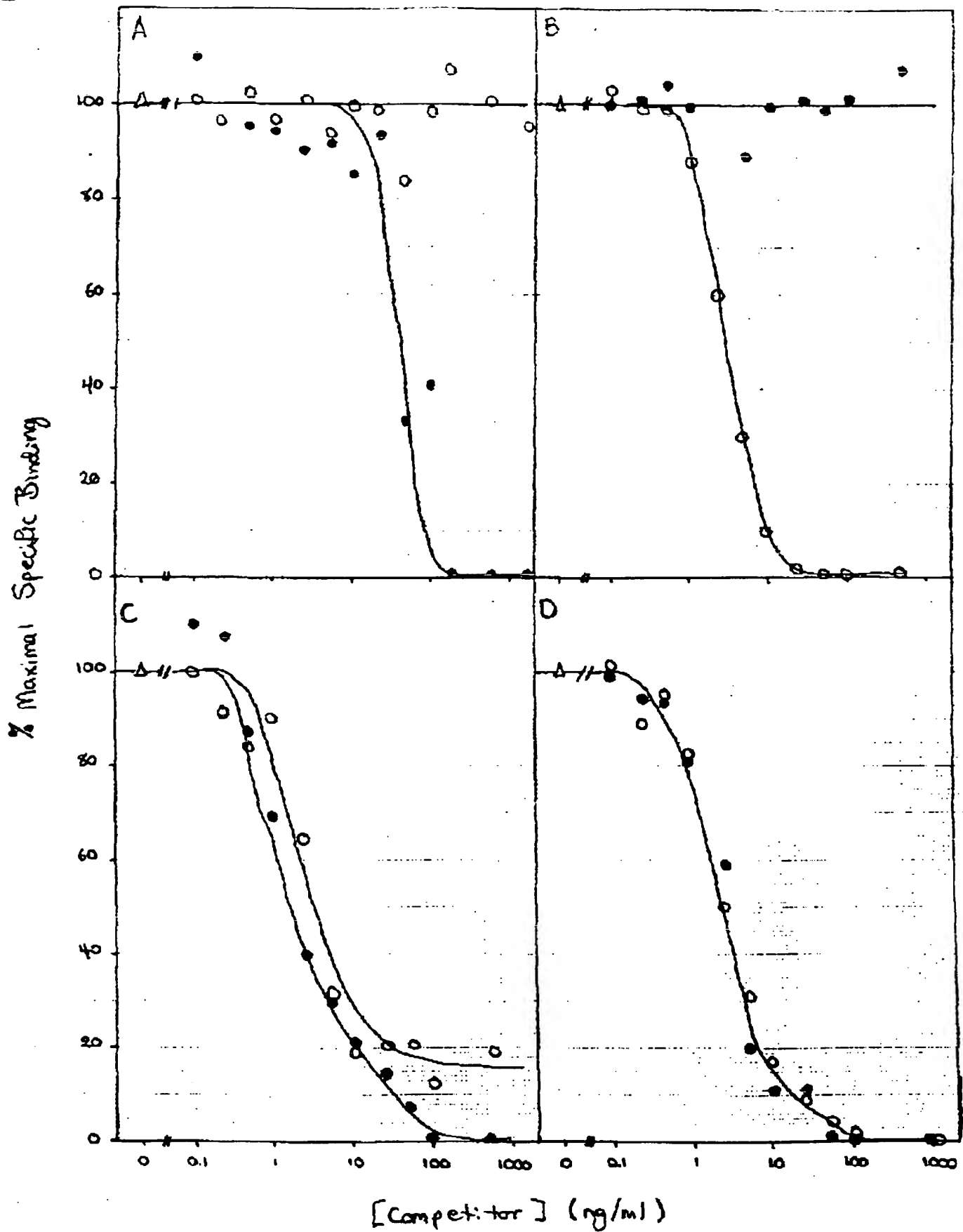


FIGURE 4

7. Maximum Number of Viable Cells.

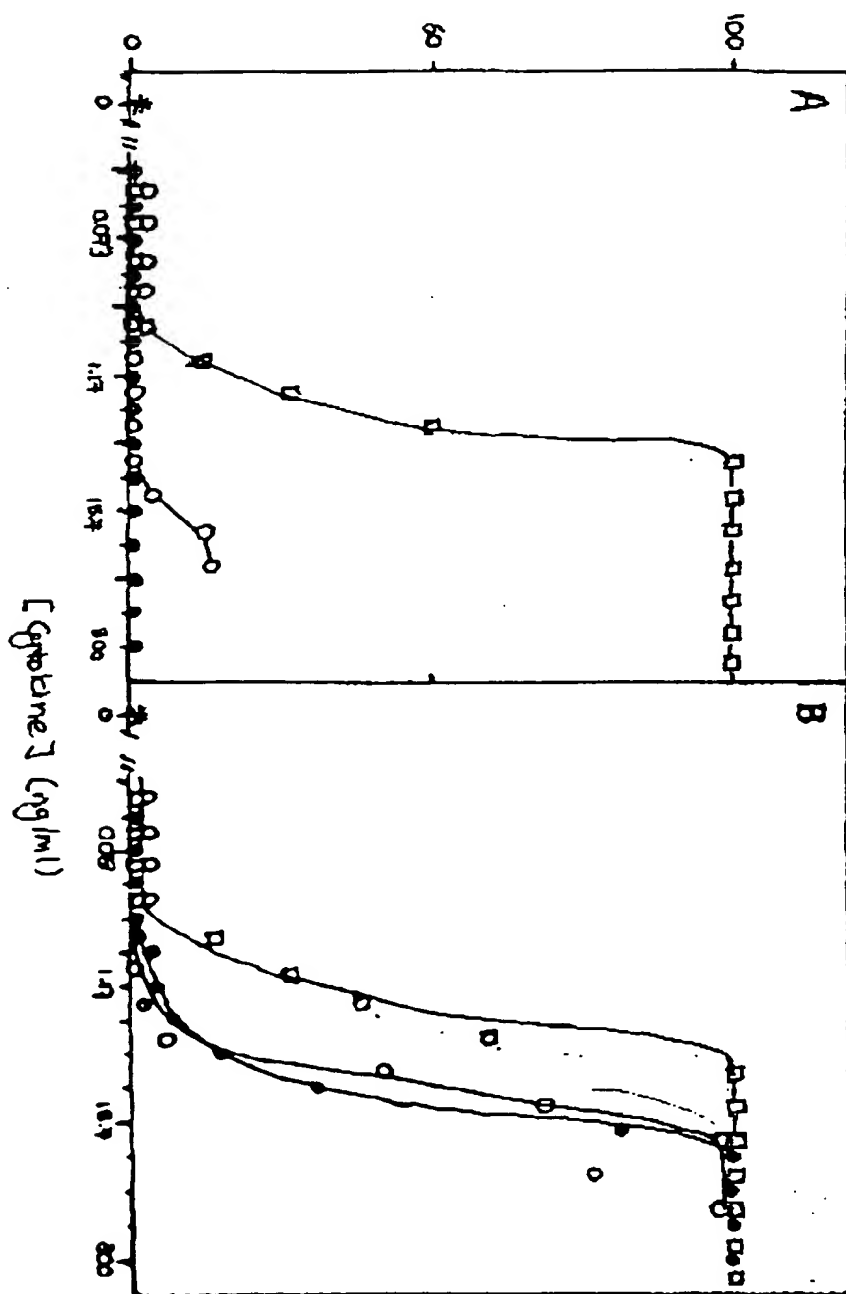


FIGURE 5

FIGURE 6

Cross-species conservation of the NR-4 (IL-13R α) gene

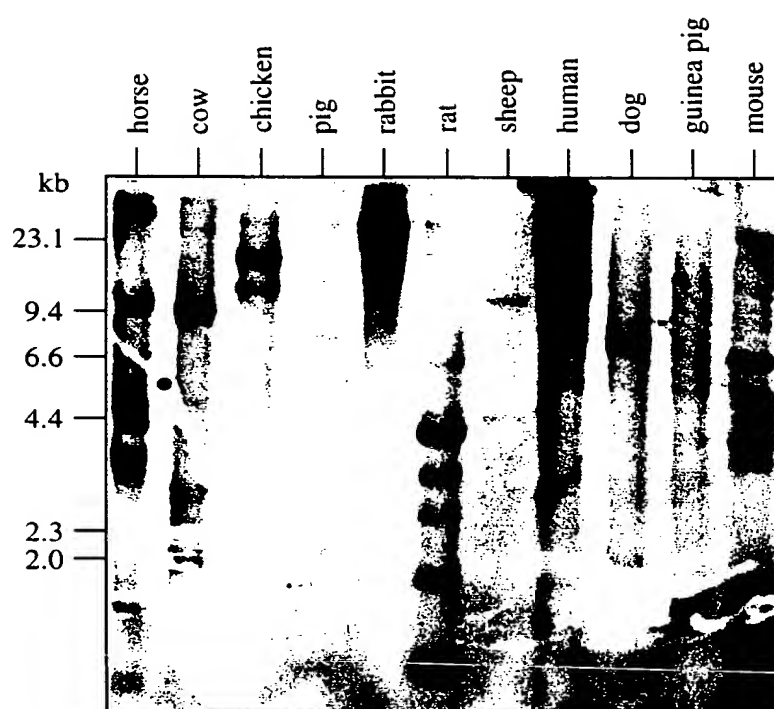


FIGURE 7

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M  -60  tgaaaagatagaataaaatggcctcgtgccgaattcggcacgagccgagggcgagggcctgc

M  1    ATGGCGCGGCCAGCGCTGCTGGGCGAGCTGTTGGTGCTGCTACTGTGGACCGCCACCGTG
M  1    M A R P A L L G E L L V L L L W T A T V

H          A P T E T Q P P V T N L S V S V
H          GCGCCTACGGAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTT
          * * * * *
M  61    GGCCAAGTTGCCGCGGCCACAGAAGTTCAGCCACCTGTGACGAATTTGAGCGTCTCTGTC
M  21    G Q V A A A T E V Q P P V T N L S V S V

H          E N L C T V I W T W N P P E G A S S N C
H          GAAAACCTCTGCACAGTAATATGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTTG
          * * * * *
M  121   GAAAATCTCTGCACGATAATATGGACGTGGAGTCTCTCTGAAGGAGCCAGTCCAAATTTG
M  41    E N L C T I I W T W S P P E G A S P N C

H          S L W Y F S H F G D K Q D K K I A P E T
H          AGTCTATGGTATTTTAGTCATTTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACT
          * * * * *
M  181   ACTCTCAGATATTTTAGTCATTTGATGACCAACAGGATAAGAAAATTGCTCCAGAAACT
M  61    T L R Y F S H F D D Q Q D K K I A P E T

H          R R S I E V P L N E R I C L Q V G S Q C
H          CGTCGTTCAATAGAAGTACCCCTGAATGAGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
          * * * * *
M  241   CATCGTAAAGAGGAATTACCCCTGGATGAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
M  81    H R K E E L P L D E K I C L Q V G S Q C

H          S T N E S E K P S I L V E K C I S P P E
H          AGCACCAATGAGAGTGAGAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCCAGAA
          * * * * *
M  301   AGTGCCAATGAAAGTGAGAAGCCTAGCCCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
M  101   S A N E S E K P S P L V K K C I S P P E

H          G D P E S A V T E L Q C I W H N L S Y M
H          GGTGATCCTGAGTCTGCTGTGACTGAACTTCAATGCATTTGGCACAACCTGAGCTACATG
          * * * * *
M  361   GGTGATCCTGAGTCCGCTGTGACTGAGCTCAAGTGCATTTGGCATAACCTGAGCTATATG
M  121   G D P E S A V T E L K C I W H N L S Y M

H          K C S W L P G R N T S P D T N Y T L Y Y
H          AAGTGTTCTTGGCTCCCTGGAAGGAATACCAGTCCCGACACTAACTATACTCTCTACTAT
          * * * * *
M  421   AAGTGTTCTTGGCTCCCTGGAAGGAATACAAGCCCTGACACACACTATACTCTGTACTAT
M  141   K C S W L P G R N T S P D T H Y T L Y Y

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FIGURE 7 (continued...)

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H      W H R S L E K I H Q C E N I F R E G Q Y
H      TGGCACAGAAGCCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATAC
      * * * * *
M 481  TGGTACAGCAGCCTGGAGAAAAGTCGTCAATGTGAAAACATCTATAGAGAAGGTCAACAC
M 161  W Y S S L E K S R Q C E N I Y R E G Q H

H      F G C S F D L T K V K D S S F E Q H S V
H      TTTGGTTGTTTCCTTTGATCTGACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTC
      * * * * *
M 541  ATTGCTTGTTTCCTTTAAATTGACTAAAGTGGAAACCT---AGTTTTGAACATCAGAACGTT
M 181  I A C S F K L T K V E P - S F E H Q N V

H      Q I M V K D N A G K I K P S F N I V P L
H      CAAATAATGGTCAAGGATAATGCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTA
      * * * * *
M 601  CAAATAATGGTCAAGGATAATGCTGGGAAAATTAGGCCATCCTGCAAAATAGTGTCTTTA
M 201  Q I M V K D N A G K I R P S C K I V S L

H      T S R V K P D P P H I K N L S F H N D D
H      ACTTCCCGTGTGAAACCTGATCCTCCACATATTAAAAACCTCTCCTTCCACAATGATGAC
      * * * * *
M 661  ACTTCTATGTGAAACCTGATCCTCCACATATTAAACATCTTCTCCTCAAAAATGGTGCC
M 221  T S Y V K P D P P H I K H L L L K N G A

H      L Y V Q W E N P Q N F I S R C L F Y E V
H      CTATATGTGCAATGGGAGAATCCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTA
      * * * * *
M 721  TTATTAGTGCAGTGAAGAATCCACAAAATTTTAGAAGCAGATGCTTAACCTTATGAAGTG
M 241  L L V Q W K N P Q N F R S R C L T Y E V

H      E V N N S Q T E T H N V F Y V Q E A K C
H      GAAGTCAATAACAGCCAAACTGAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGT
      * * * * *
M 781  GAGGTCAATAATACTCAAACCGACCGACATAATTTTTAGAGGTTGAAGAGGACAAATGC
M 261  E V N N T Q T D R H N I L E V E E D K C

H      E N P E F E R N V E N T S C F M V P G V
H      GAGAATCCAGAATTTGAGAGAAATGTGGAGAATACATCTTGTTTCATGGTCCCTGGTGTT
      * * * * *
M 841  CAGAATTCGAATCTGATAGAAACATGGAGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
M 281  Q N S E S D R N M E G T S C F Q L P G V

H      L P D T L N T V R I R V K T N K L C Y E
H      CTTCTGATACTTTGAACACAGTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAG
      * * * * *
M 901  CTTGCCGACGCTGTCTACACAGTCAGAGTAAGAGTCAAAACAAACAAGTTATGCTTTGAT
M 301  L A D A V Y T V R V R V K T N K L C F D

H      D D K L W S N W S Q E M S I G K K R N S
H      GATGACAAACTCTGGAGTAATTGGAGCCAAGAAATGAGTATAGGTAAGAGCGCAATTCC
      * * * * *
M 961  GACAACAAACTGTGGAGTGATTGGAGTGAAGCACAGAGTATAGGTAAGGAGCAAACTCC
M 321  D N K L W S D W S E A Q S I G K E Q N S

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FIGURE 7 (continued...)

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H      T L Y I T M L L I V P V I V A G A I I V
H      ACACTCTACATAACCATGTTACTCATTGTTCCAGTCATCGTCGCAGGTGCAATCATAGTA
      * * * * *
M 1021 ACCTTCTACACCACCATGTTACTCACCATTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
M 341  T F Y T T M L L T I P V F V A V A V I I

H      L L L Y L K R L K I I I F P P I P D P G
H      CTCCTGCTTTACCTAAAAAGGCTCAAGATTATTATATTCCCTCCAATTCCTGATCCTGGC
      * * * * *
M 1081 CTCCTTTTTTACCTGAAAAGGCTTAAGATCATTATATTTCCCTCCAATTCCTGATCCTGGC
M 361  L L F Y L K R L K I I I F P P I P D P G

H      K I F K E M F G D Q N D D T L H W K K Y
H      AAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTAC
      * * * * *
M 1141 AAGATTTTTAAAGAAATGTTTGGAGACCAGAATGATGATACCCTGCACTGGAAGAAGTAT
M 381  K I F K E M F G D Q N D D T L H W K K Y

H      D I Y E K Q T K E E T D S V V L I E N L
H      GACATCTATGAGAAGCAAACCAAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTG
      * * * * *
M 1201 GACATCTATGAGAAACAATCCAAAGAAGAAACGGATTCTGTAGTGCTGATAGAAAACCTG
M 401  D I Y E K Q S K E E T D S V V L I E N L

H      K K A S Q *
H      AAGAAAGCCTCTCAGTGAtggagataattttatttttaccttcactgtgaccttgagaaga
      * * *
M 1261 AAGAAAGCAGCTCCTTGAtggggagaagtgatttccttcttgcccttcaatgtgaccctgt
M 421  K K A A P *

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FIGURE 8

NR4 expression in mouse tissues

